a1

b) obtaining a mutant genomic DNA sample from at least one of said organisms exhibiting said mutant phenotype and a wild-type genomic DNA sample from at least one of said organisms not exhibiting said mutant phenotype;

c) fragmenting at least one of said mutant and at least one of said wild-type genomic DNA samples to produce DNA fragments;

d) attaching an adapter to at least one of said mutant DNA fragments and to at least one of said wild-type DNA fragments, resulting in a collection of adapter-modified DNA fragments;

e) amplifying said mutant and wild-type adapter-modified DNA fragments to yield amplification products comprising said genetic sequence, wherein said amplification employs a first oligonucleotide primer which selectively hybridizes under stringent hybridization conditions to said adapter sequence, and a second oligonucleotide primer which selectively hybridizes under stringent hybridization conditions to said transposable element; and,

f) isolating an amplification product present in said organism exhibiting said mutant phenotype and absent in said organism not exhibiting said mutant phenotype, wherein said isolated amplification product comprises said genetic sequence associated with said mutant phenotype.

a2

6. (Amended) The method of claim 5, wherein *Mutator*-TIR is a template for said second oligonucleotide primer.

a3 Sub C

9. (Amended) ~~The~~ method of claim 1, further comprising a second amplification to preferentially amplify adapter-modified DNA fragments, wherein said second amplification

a3 employs at least two oligonucleotide primers, with one of said primers selectively hybridizing under stringent hybridization conditions to said adapter sequence, and the other primer selectively hybridizing under stringent hybridization conditions to said transposable element.

10. (Amended) The method of claim 9, wherein said primers of said second amplification are nested within said primers of step (e) of claim 1.

11. (Amended) The method of claim 1, wherein said amplification of step (e) is achieved by polymerase chain reaction (PCR).

12. (Amended) The method of claim 1, wherein said fragmentation of step (c) is achieved by digestion with at least one restriction enzyme.

13. (Amended) The method of claim 1, wherein said mutant genomic DNA sample of step (b) comprises genomic DNA from at least 2 organisms and said wild-type genomic DNA sample comprises genomic DNA of at least 10 organisms.

14. (Amended) The method of claim 1, wherein at least one of said oligonucleotide primers is labeled.

15. (Amended) A method for identifying one or more locations of a genomic insertion by a transgene in genomic DNA of an organism, said method comprising the following steps:

a) isolating a genomic DNA sample from said organism;

b) fragmenting said isolated genomic DNA sample to yield a collection of DNA fragments;

c) attaching an adapter sequence to at least one of said DNA fragments to yield a collection of adapter-modified DNA fragments;